STIC Search Report
Biotech-Chem Library

USPTO

STIC Database Tracking Number: 139816

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Wednesday, December 08, 2004

Case Serial Number: 09/747385

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From: Lambertson, David

Sent: Tuesday, December 07, 2004 12:47 PM

To: O'Bryen, Barbara

Cc: Lambertson, David

Subject: Search Request

Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	Remsen 02B79
Mailbox room#:	Remsen 02C70
Phone:	(571) 272-0771
Results Format:	paper

Serial #:09/747, 385

Please Search:

Nucleic Acid databases for:

SEQ ID No: 2-4 (1224 nt, 32 nt, and 132 nt, respectively)

Including:

1. Interference Search.

Also,

Protein and Nucleic Acid databases for:

SEQ ID NO: 1 (407 aa)

Including:

1. Interference Search.

Thanks,

12/7/04

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                GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    December 7, 2004, 22:53:52 ; Search time 102.496 Seconds
                                         (without alignments)
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Title:          US-09-747-385-4
Perfect score:  132
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters:       7390102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	39.2	29.7	2000	16	US-10-260-238-2019	Sequence 2019, Ap
c 5	38.8	29.4	380	17	US-10-437-963-37068	Sequence 37068, A
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c 9	36.6	27.9	19787	15	US-10-311-455-1424	Sequence 1424, Ap
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c 15	36	27.3	2000	16	US-10-260-238-2019	Sequence 2019, Ap
16	36	27.3	17538	15	US-10-311-455-1130	Sequence 1130, Ap
c 17	36	27.3	344805	18	US-10-779-271-1	Sequence 1, Appli
c 18	35.6	27.0	56153	16	US-10-221-714A-520	Sequence 520, App
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21	34.4	26.1	5379	15	US-10-311-455-1650	Sequence 1650, App
22	34.4	26.1	5379	15	US-10-240-485-130	Sequence 130, App
23	34.4	26.1	8576	15	US-10-311-455-2201	Sequence 2201, Ap
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26	34.2	25.9	12590	15	US-10-311-455-1894	Sequence 1894, Ap
27	34.2	25.9	45862	13	US-10-216-355-3	Sequence 3, Appli
28	34	25.8	7047	15	US-10-240-453-259	Sequence 259, App
29	34	25.8	10183	16	US-10-221-714-478	Sequence 478, App
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31	33.8	25.6	1288	16	US-10-425-114-12969	Sequence 12969, A
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33	33.8	25.6	16228	16	US-10-221-613-87	Sequence 387, App
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c 42	33.4	25.3	5507	18	US-10-473-126-344	Sequence 344, App
c 43	33.4	25.3	6308	15	US-10-311-455-1444	Sequence 1444, Ap
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ALIGNMENTS

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; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5765
; LENGTH: 24617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-5765

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Best Local Similarity  60.3%;
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Db  19206 AGATTTACTTTATATACAGGGCAAAAGTAAATCATACAGACCCATTTGTCAATTTTA 19265

Qy     77 CAGGACAAATTTCAACTTTAACAGGACAAATTTCAACTTTAACAGGACAAATTT 132
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Db  19266 TTTTTGAATTTAAATTTAAAGGGACAAATACTTCATTTTAACAAGGTATATGT 19321

RESULT 2
US-10-311-455-567
; Sequence 567, Application US/10311455
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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:     December 7, 2004, 21:22:51 ; Search time 18.6792 Seconds
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Perfect score: 132
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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7	32.8	24.8	6072	3	US-09-535-381-3	Sequence 3, Appli
8	32.2	24.4	5804	4	US-08-956-171E-249	Sequence 249, App
9	32.2	24.4	5804	4	US-08-781-986A-249	Sequence 249, App
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11	32	24.2	1308	3	US-09-601-198-3	Sequence 3, Appli
12	32	24.2	6306	4	US-10-204-708-50	Sequence 50, Appl
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23	31	23.5	1888	3	US-09-035-648-20	Sequence 20, Appl
24	31	23.5	1888	3	US-09-001-951-20	Sequence 20, Appl
25	31	23.5	1888	4	US-08-818-829-20	Sequence 20, Appl
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27	30.8	23.3	8353	3	US-08-611-587-1	Sequence 1, Appli
28	30.8	23.3	319608	4	US-09-539-333D-1	Sequence 1, Appli
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ALIGNMENTS

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; Patent No. 6114605
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; GENERAL INFORMATION:
;  APPLICANT: Williamson, Valerie M.
;  APPLICANT: Kaloshian, Isgouhi
;  APPLICANT: Yaghoobi, Jafar
;  APPLICANT: Bodeau, John
;  APPLICANT: Milligan, Stephen
;  TITLE OF INVENTION: Procedures and Materials for Conferring
;  TITLE OF INVENTION: Pest Resistance in Plants
;  NUMBER OF SEQUENCES: 5
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
;  COMPUTER READABLE FORM:
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;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
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;   APPLICATION NUMBER: US/08/947,823
;   FILING DATE: 09-OCT-1997
;   CLASSIFICATION: 800
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US97/18802
;   FILING DATE: 09-OCT-1997
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/028,191
;   FILING DATE: 10-OCT-1996
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Bastian, Kevin L.
;   REGISTRATION NUMBER: 34,774
;   REFERENCE/DOCKET NUMBER: 023070-070210US
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 51952 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-08-947-823-1
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 22:53:52 ; Search time 17.0827 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters: 7390102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Published Applications NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	6	17.4	79.1	1087	13	US-10-027-632-9376	Sequence 9376, Ap
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	8	17.2	78.2	1254	16	US-10-282-122A-36263	Sequence 36263, A
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	16	17.2	78.2	828	15	US-10-012-697-85	Sequence 85, Appl
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	18	17.2	78.2	873	13	US-10-027-632-172294	Sequence 172294,
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c	40	16.8	76.4	182	18	US-10-425-115-150471	Sequence 150471,
c	41	16.8	76.4	476	13	US-10-027-632-45431	Sequence 45431, A
c	42	16.8	76.4	476	15	US-10-027-632-45431	Sequence 45431, A
c	43	16.8	76.4	488	13	US-10-027-632-265888	Sequence 265888,
c	44	16.8	76.4	488	15	US-10-027-632-265888	Sequence 265888,
c	45	16.8	76.4	684	13	US-10-027-632-126537	Sequence 126537,

ALIGNMENTS

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US-10-032-585-6022
; Sequence 6022, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6022
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-6022

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Matches 20;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

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RESULT 2
US-10-398-221-3733
; Sequence 3733, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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3	17.2	78.2	442	4	US-09-513-999C-2604	Sequence 2604, Ap
4	17.2	78.2	450	4	US-09-248-796A-3551	Sequence 3551, Ap
c 5	17.2	78.2	3083	2	US-08-480-994-36	Sequence 36, Appl
c 6	17.2	78.2	3083	2	US-08-616-844-36	Sequence 36, Appl
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c 8	17.2	78.2	3083	3	US-08-485-573-36	Sequence 36, Appl
c 9	17.2	78.2	3083	3	US-08-944-868A-36	Sequence 36, Appl
c 10	17.2	78.2	3083	3	US-08-944-423A-36	Sequence 36, Appl
c 11	17.2	78.2	3083	3	US-08-925-743-36	Sequence 36, Appl
c 12	17.2	78.2	3083	3	US-08-944-496-36	Sequence 36, Appl
c 13	17.2	78.2	3083	3	US-08-925-767-36	Sequence 36, Appl
c 14	17.2	78.2	3084	3	US-08-826-246-11	Sequence 11, Appl
c 15	17.2	78.2	3084	3	US-08-944-495-11	Sequence 11, Appl
c 16	17.2	78.2	3084	4	US-09-126-640-6	Sequence 6, Appli
c 17	17.2	78.2	3084	4	US-08-925-588-11	Sequence 11, Appl
c 18	17.2	78.2	3084	4	US-09-288-292A-6	Sequence 6, Appli
c 19	17.2	78.2	3084	4	US-09-372-044-11	Sequence 11, Appl
c 20	17.2	78.2	3084	4	US-08-825-486-11	Sequence 11, Appl
c 21	17.2	78.2	3084	4	US-08-826-248-11	Sequence 11, Appl
c 22	17.2	78.2	8022	4	US-09-029-047C-3	Sequence 3, Appli
c 23	17.2	78.2	9834	4	US-08-956-171E-37	Sequence 37, Appl
c 24	17.2	78.2	9834	4	US-08-781-986A-37	Sequence 37, Appl
c 25	16.8	76.4	1863	4	US-09-248-796A-2811	Sequence 2811, Ap
c 26	16.8	76.4	1914	4	US-09-690-454-34	Sequence 34, Appl
c 27	16.8	76.4	6990	4	US-09-620-312D-155	Sequence 155, App

c 28	16.4	74.5	250	4	US-09-513-999C-23096	Sequence 23096, A
29	16.4	74.5	844	4	US-08-956-171E-619	Sequence 619, App
30	16.4	74.5	844	4	US-08-781-986A-619	Sequence 619, App
c 31	16.4	74.5	4011	1	US-08-121-057-3	Sequence 3, Appli
c 32	16.4	74.5	4011	2	US-08-509-187D-3	Sequence 3, Appli
c 33	16.4	74.5	4011	2	US-09-121-396-3	Sequence 3, Appli
c 34	16.4	74.5	4011	5	PCT-US93-09704A-3	Sequence 3, Appli
c 35	16.4	74.5	786431	4	US-09-751-389-3	Sequence 3, Appli
c 36	16.2	73.6	369	4	US-09-513-999C-36236	Sequence 36236, A
c 37	16.2	73.6	445	4	US-09-621-976-18137	Sequence 18137, A
38	16.2	73.6	499	4	US-09-679-409-56	Sequence 56, Appl
c 39	16.2	73.6	1200	2	US-08-747-887-1	Sequence 1, Appli
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41	16.2	73.6	1563	4	US-09-328-352-2466	Sequence 2466, Ap
42	16.2	73.6	2224	1	US-08-261-086-3	Sequence 3, Appli
c 43	16.2	73.6	2380	4	US-09-270-767-5110	Sequence 5110, Ap
c 44	16.2	73.6	2380	4	US-09-270-767-20392	Sequence 20392, A
c 45	16.2	73.6	3001	4	US-09-539-333D-126	Sequence 126, App

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; Sequence 5223, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5223
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5223

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; Sequence 21, Application US/09792024
; Patent No. 6783985
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; TITLE OF INVENTION: Targets Discovery
; FILE REFERENCE: 10182-004-999
; CURRENT APPLICATION NUMBER: US/09/792,024
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 490
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 984
; TYPE: DNA
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         Copyright (c) 1993 - 2004 Compugen Ltd.

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c 2	175.8	14.4	6668	15	US-10-311-455-1670	Sequence 1670, Ap
c 3	173	14.1	3673778	15	US-10-312-841-1	Sequence 1, Appli
c 4	167.6	13.7	7442	16	US-10-221-714A-409	Sequence 409, App
c 5	166.2	13.6	7597	15	US-10-311-455-986	Sequence 986, App
c 6	166	13.6	6292	16	US-10-221-714A-461	Sequence 461, App
c 7	162.2	13.3	3683	15	US-10-311-455-339	Sequence 339, App
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c 9	156.6	12.8	3683	18	US-10-473-126-193	Sequence 193, App
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c 11	152.8	12.5	1297	18	US-10-425-115-67687	Sequence 67687, A
c 12	152.4	12.5	15387	15	US-10-311-455-157	Sequence 157, App
c 13	151.6	12.4	8056	18	US-10-473-126-386	Sequence 386, App
c 14	151.4	12.4	1243	18	US-10-425-115-172717	Sequence 172717,
c 15	150.6	12.3	975	18	US-10-363-345A-16099	Sequence 16099, A
c 16	150.6	12.3	975	18	US-10-363-345A-16100	Sequence 16100, A
c 17	148.4	12.1	1204	17	US-10-437-963-77858	Sequence 77858, A
c 18	148.4	12.1	8056	18	US-10-473-126-386	Sequence 386, App
c 19	148	12.1	8056	18	US-10-473-126-240	Sequence 240, App
c 20	147	12.0	14006	15	US-10-311-455-1931	Sequence 1931, Ap
c 21	146.4	12.0	1081	18	US-10-425-115-16756	Sequence 16756, A
c 22	145.6	11.9	1062	18	US-10-425-115-120013	Sequence 120013,
c 23	144	11.8	17967	15	US-10-311-455-988	Sequence 988, App
c 24	143.4	11.7	5413	15	US-10-311-455-537	Sequence 537, App
c 25	143.2	11.7	1004	18	US-10-425-115-81106	Sequence 81106, A
c 26	143	11.7	7571	15	US-10-311-455-500	Sequence 500, App
c 27	142.6	11.7	9539	14	US-10-239-676-51	Sequence 51, Appl
c 28	142.6	11.6	9539	15	US-10-240-453-53	Sequence 53, Appl
c 29	142.2	11.6	9964	15	US-10-311-455-71	Sequence 71, Appl
c 30	141.8	11.6	1130	18	US-10-425-115-132399	Sequence 132399,
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c 34	140	11.4	18154	15	US-10-311-455-227	Sequence 227, App
c 35	139.4	11.4	1039	18	US-10-425-115-58802	Sequence 58802, A
c 36	139.2	11.4	996	18	US-10-425-115-151933	Sequence 151933,
c 37	137.8	11.3	8056	18	US-10-473-126-240	Sequence 240, App
c 38	137.8	11.3	83391	17	US-10-433-793-123	Sequence 123, App
c 39	137.2	11.2	778	18	US-10-363-345A-2179	Sequence 2179, Ap
c 40	137.2	11.2	778	18	US-10-363-345A-2180	Sequence 2180, Ap
c 41	137.2	11.2	9539	14	US-10-239-676-52	Sequence 52, Appl
c 42	137.2	11.2	9539	15	US-10-240-453-54	Sequence 54, Appl
c 43	136.8	11.2	5276	15	US-10-311-455-124	Sequence 124, Appl
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; Publication No. US20040110205A1
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; APPLICANT: Agilent Technologies
; TITLE OF INVENTION: Methods and Systems for Nanopore Data Analysis
; FILE REFERENCE: 50112-1580
; CURRENT APPLICATION NUMBER: US/10/668,749A
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-668-749A-1

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Qy   136 TTTTTATTTGAAAAATTCATAAATGATTTAGATAATAATACTTTAACTATAAGAGTAACA 195
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                GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

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and is derived by analysis of the total score distribution.
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	5	107	8.7	6669	4	US-10-204-708-6	Sequence 6, Appli
c	6	106.8	8.7	3095	6	5231168-1	Patent No. 5231168
	7	104.8	8.6	5562	4	US-10-204-708-63	Sequence 63, Appl
c	8	104.6	8.5	6124	4	US-08-213-419B-3	Sequence 3, Appli
	9	103.4	8.4	640681	4	US-09-790-988-1	Sequence 1, Appli
	10	101.6	8.3	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	11	101.6	8.3	1664976	4	US-09-692-570-1	Sequence 1, Appli
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	14	100.8	8.2	1956	4	US-08-559-896B-1	Sequence 1, Appli
	15	100.8	8.2	1956	4	US-09-351-794A-1	Sequence 1, Appli
	16	100.6	8.2	4766	5	PCT-US93-07261-10	Sequence 10, Appl
	17	100.4	8.2	10640	4	US-09-417-485D-5	Sequence 5, Appli
	18	99.8	8.2	6152	3	US-09-973-462-1	Sequence 1, Appli
	19	98	8.0	5152	4	US-10-204-708-73	Sequence 73, Appl
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	25	95.2	7.8	11049	4	US-10-204-708-23	Sequence 23, Appl
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c	28	94	7.7	6070	4	US-10-204-708-10	Sequence 10, Appl
c	29	93	7.6	5455	4	US-10-204-708-33	Sequence 33, Appl
c	30	93	7.6	6156	4	US-10-204-708-60	Sequence 60, Appl
c	31	92.6	7.6	6866	4	US-10-204-708-20	Sequence 20, Appl
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c	33	91.2	7.5	6317	4	US-10-204-708-11	Sequence 11, Appl
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	43	87.2	7.1	6113	4	US-10-204-708-14	Sequence 14, Appl
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ALIGNMENTS

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; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
;  APPLICANT:  Sim, Kim L.
;  APPLICANT:  Chitnis, Chetan
;  APPLICANT:  Miller, Louis H.
;  APPLICANT:  Peterson, David S.
;  APPLICANT:  Su, Xin-zhaun
;  APPLICANT:  Wellems, Thomas E.
;  TITLE OF INVENTION:  BINDING DOMAINS FROM PLASMODIUM VIVAX
;  TITLE OF INVENTION:  AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;  NUMBER OF SEQUENCES:  45
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE:  Knobbe Martens Olson & Bear
;  STREET:  620 Newport Center Drive  16th Floor
;  CITY:  Newport Beach
;  STATE:  California
;  COUNTRY:  US
;  ZIP:  92660
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE:  Floppy disk
;  COMPUTER:  IBM PC compatible
;  OPERATING SYSTEM:  PC-DOS/MS-DOS
;  SOFTWARE:  PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER:  US/08/487,826B
;  FILING DATE:  10-SEP-1993
;  CLASSIFICATION:  435
;  ATTORNEY/AGENT INFORMATION:
;  NAME:  Israelsen, Ned
;  REGISTRATION NUMBER:  29,655
;  REFERENCE/DOCKET NUMBER:  NIH121.001CP1
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE:  (619) 235-8550
;  TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  13:
;  SEQUENCE CHARACTERISTICS:
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;  TYPE:  nucleic acid
;  STRANDEDNESS:  single
;  TOPOLOGY:  linear
;  MOLECULE TYPE:  cDNA
;  HYPOTHETICAL:  NO
;  ANTI-SENSE:  NO
US-08-487-826B-13

Query Match                 9.4%;  Score 114.8; DB 2; Length 19124;
Best Local Similarity      49.8%;  Pred. No. 9e-11;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	198.5	9.6	5528	16	US-10-415-253-1	Sequence 1, Appli
6	198.5	9.6	6152	9	US-09-742-096-1	Sequence 1, Appli
7	196	9.4	3510	15	US-10-369-493-24782	Sequence 24782, A
8	193.5	9.3	3475	10	US-09-883-343A-15	Sequence 15, Appl
9	193.5	9.3	3393	15	US-10-117-937-597	Sequence 597, Appl
10	192.5	9.3	3393	15	US-10-657-022-93	Sequence 93, Appl
11	191.5	9.2	2564	18	US-10-416-330-12	Sequence 12, Appl
12	190	9.2	3546	16	US-10-282-122A-17261	Sequence 17261, A
13	189	9.1	3492	16	US-10-282-122A-15680	Sequence 15680, A
14	188.5	9.1	2853	16	US-10-282-122A-11101	Sequence 11101, A
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19	183.5	8.8	2280	16	US-10-335-977-3932	Sequence 3932, Ap
20	183.5	8.8	2286	16	US-10-335-977-3933	Sequence 3933, Ap
21	183.5	8.8	2341	9	US-09-881-752A-147	Sequence 147, App
22	182	8.8	5847	15	US-10-032-585-6611	Sequence 6611, Ap
23	181.5	8.7	2643	15	US-10-369-493-45330	Sequence 45330, A
24	181.5	8.7	5641	15	US-10-032-585-6646	Sequence 6646, Ap
25	181	8.7	3588	16	US-10-282-122A-16553	Sequence 16553, A
26	181	8.7	4410	17	US-10-473-576-25	Sequence 25, Appl
27	180.5	8.7	5628	15	US-10-369-493-45972	Sequence 45972, A
28	180	8.7	3378	16	US-10-282-122A-11029	Sequence 11029, A
29	179.5	8.6	2232	14	US-10-087-464-45	Sequence 45, Appl
30	179.5	8.6	6386	13	US-10-098-841-40	Sequence 40, Appl
31	178	8.6	2728	16	US-10-302-172-62	Sequence 62, Appl
32	178	8.6	3471	15	US-10-369-493-23730	Sequence 23730, A
33	178	8.6	4350	17	US-10-473-576-45	Sequence 45, Appl
34	177.5	8.5	2171	18	US-10-416-330-6	Sequence 6, Appli
35	177.5	8.5	3552	16	US-10-282-122A-17070	Sequence 17070, A
36	176	8.5	5967	15	US-10-171-581-158	Sequence 158, App
37	173	8.3	2061	16	US-10-282-122A-21613	Sequence 21613, A
38	173	8.3	3624	13	US-10-108-605-216	Sequence 216, App
39	172.5	8.3	2673	15	US-10-369-493-37164	Sequence 37164, A
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41	171.5	8.3	1749	16	US-10-398-221-2342	Sequence 2342, Ap
42	171.5	8.3	1755	16	US-10-398-221-652	Sequence 652, App
43	171.5	8.3	5457	16	US-10-282-122A-28061	Sequence 28061, A
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ALIGNMENTS

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; Sequence 24748, Application US/10369493
; Publication No. US2003023367SA1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 24748
; LENGTH: 3018
; TYPE: DNA

GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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13	178	8.6	2728	4	US-09-799-451-62	Sequence 62, Appl
14	178	8.6	3763	1	US-07-107-865D-1	Sequence 1, Appli
15	175	8.4	2133	4	US-09-107-532A-1413	Sequence 1413, Ap
16	172.5	8.3	3237	4	US-09-248-796A-6181	Sequence 6181, Ap
17	172	8.3	2229	4	US-09-248-796A-4950	Sequence 4950, Ap
18	171.5	8.3	2775	4	US-09-248-796A-4695	Sequence 4695, Ap
19	169.5	8.2	3636	3	US-09-134-001C-1983	Sequence 1983, Ap
20	168.5	8.1	2718	4	US-09-248-796A-2230	Sequence 2230, Ap
21	168	8.1	3033	3	US-09-134-001C-2341	Sequence 2341, Ap
22	167	8.0	9626	3	US-09-150-867-2	Sequence 2, Appli
23	166.5	8.0	3294	3	US-08-923-992A-7	Sequence 7, Appli
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ALIGNMENTS

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; APPLICANT: Bult et al.
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; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1996-08-22
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	* Score	% Match	Query Match Length	DB	ID	Description
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5	198.5	9.6	1787	15	US-10-415-253-2	Sequence 2, Appli
6	196	9.4	1169	14	US-10-369-493-1095	Sequence 1095, Ap
7	192.5	9.3	976	14	US-10-117-937-596	Sequence 596, App
8	192.5	9.3	976	16	US-10-657-022-92	Sequence 92, Appl
9	191.5	9.2	795	16	US-10-408-765A-1205	Sequence 1205, Ap
10	191.5	9.2	795	17	US-10-416-330-34	Sequence 34, Appl
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14	187.5	9.0	1294	15	US-10-282-122A-61292	Sequence 61292, A
15	187.5	9.0	1805	10	US-09-820-843A-73	Sequence 73, Appl
16	187.5	9.0	1805	15	US-10-282-122A-63513	Sequence 63513, A
17	185.5	8.9	944	14	US-10-369-493-1682	Sequence 1682, Ap
18	183.5	8.8	759	15	US-10-335-977-8694	Sequence 8694, Ap
19	183.5	8.8	762	15	US-10-335-977-8695	Sequence 8695, Ap
20	181.5	8.7	880	14	US-10-369-493-21643	Sequence 21643, A
21	181.5	8.7	1881	14	US-10-032-585-7646	Sequence 7646, Ap
22	181	8.7	1196	15	US-10-282-122A-52737	Sequence 52737, A
23	181	8.7	1404	16	US-10-473-576-2	Sequence 2, Appli
24	180.5	8.7	1875	15	US-10-369-493-22285	Sequence 22285, A
25	180	8.7	1125	15	US-10-282-122A-47213	Sequence 47213, A
26	179.5	8.6	743	14	US-10-087-464-53	Sequence 53, Appl
27	178	8.6	1156	14	US-10-369-493-43	Sequence 43, Appl
28	178	8.6	1384	16	US-10-473-576-22	Sequence 22, Appl
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31	173	8.3	687	15	US-10-282-122A-57797	Sequence 57797, A
32	173	8.3	879	13	US-10-108-605-217	Sequence 217, App
33	172.5	8.3	891	14	US-10-369-493-13477	Sequence 13477, A
34	172	8.3	497	10	US-09-820-843A-32	Sequence 32, Appl
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39	170	8.2	670	9	US-09-748-875-63	Sequence 63, Appl
40	170	8.2	670	10	US-09-298-523B-63	Sequence 63, Appl
41	170	8.2	1979	14	US-10-205-823-419	Sequence 419, App
42	169	8.1	996	9	US-09-815-242-5251	Sequence 5251, Ap
43	169	8.1	1009	9	US-10-094-749-2480	Sequence 12141, A
44	168.5	8.1	567	14	US-09-815-242-12141	Sequence 2480, Ap
45	168.5	8.1	613	17	US-10-416-330-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-10-369-493-1061
; Sequence 1061, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1061
; LENGTH: 1005
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-10-369-493-1061

Query Match   11.9%; Score 247; DB 14; Length 1005;
Best Local Similarity 24.4%; Pred. No. 1.6e-05;
Matches 109; Conservative 85; Mismatches 165; Indels 88; Gaps 20;

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Db   202 QLEEKNKKLMEINDKLNKIKKEFEDIEKLFNEWENKLLYEKFINKLLEERKRALELKNQE 261

Wed Dec 8 09:08:20 2004

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              GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    December 7, 2004, 18:31:43 ; Search time 39 Seconds
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Title:         US-09-747-385-1
Perfect score: 2077
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Total number of hits satisfying chosen parameters:        478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	DB	Length	ID	Description
1	198.5	9.6	3	1786	US-08-973-462-8	Sequence 8, Appli
2	197	9.5	4	241	US-09-107-532A-4086	Sequence 4086, Ap
3	192.5	9.3	4	976	US-09-104-324B-4	Sequence 4, Appli
4	192.5	9.3	1	976	US-09-538-092-1339	Sequence 1339, Ap
5	180.5	8.7	1	740	US-08-353-700-5	Sequence 5, Appli
6	175	8.4	4	710	US-09-107-532A-5067	Sequence 5067, Ap
7	172.5	8.3	4	1078	US-09-248-796A-20284	Sequence 20284, A
8	172	8.3	4	742	US-09-248-796A-19053	Sequence 19053, A
9	171.5	8.3	4	924	US-09-248-796A-18798	Sequence 18798, A
10	169.5	8.2	4	1211	US-09-134-001C-4820	Sequence 4820, Ap
11	168.5	8.1	4	905	US-09-248-796A-16333	Sequence 16333, A
12	168	8.1	3	1010	US-09-134-001C-5178	Sequence 5178, Ap
13	167	8.0	1	2954	US-09-150-867-1	Sequence 1, Appli
14	166.5	8.0	3	1098	US-08-923-992A-8	Sequence 8, Appli
15	163	7.8	4	630	US-09-248-796A-20275	Sequence 20275, A
16	162	7.8	4	810	US-09-248-796A-20281	Sequence 20281, A
17	162	7.8	4	1427	US-09-538-092-1044	Sequence 1044, Ap
18	161	7.8	3	1128	US-08-923-992A-6	Sequence 6, Appli
19	161	7.8	3	1164	US-09-750-590-2	Sequence 2, Appli
20	161	7.8	1	1401	US-08-220-958-2	Sequence 2, Appli
21	160.5	7.7	1	384	US-09-308-375-2	Sequence 2, Appli
22	160.5	7.7	3	2285	US-09-595-684B-31	Sequence 31, Appl
23	160.5	7.7	2	2663	US-09-538-092-1252	Sequence 1252, Ap
24	160.5	7.7	4	2663	US-09-722-139-2	Sequence 2, Appli
25	160	7.7	3	1375	US-09-721-832-2	Sequence 2, Appli
26	160	7.7	2	1375	US-09-721-689-2	Sequence 2, Appli
27	160	7.7	4	1375		
28	159.5	7.7	3	1354	US-08-685-871-2	Sequence 2, Appli
29	159.5	7.7	1	2482	US-08-328-254-6	Sequence 6, Appli
30	159.5	7.7	4	3210	US-09-538-092-1154	Sequence 1154, Ap
31	159	7.7	4	472	US-09-166-350-17	Sequence 17, Appl
32	158.5	7.6	4	583	US-09-710-279-1358	Sequence 1358, Ap
33	158.5	7.6	5	3248	US-08-353-700-1	Sequence 1, Appli
34	158.5	7.6	2	3248	PCT-US95-16216-1	Sequence 1, Appli
35	158	7.6	2	645	US-08-592-126-144	Sequence 144, App
36	158	7.6	4	645	US-08-687-080-47	Sequence 47, Appl
37	158	7.6	4	645	US-09-168-595-144	Sequence 144, App
38	158	7.6	4	668	US-09-328-352-6586	Sequence 6586, Ap
39	158	7.6	2	1312	US-08-592-126-148	Sequence 148, App
40	158	7.6	2	1312	US-08-687-080-51	Sequence 51, Appl
41	158	7.6	4	1312	US-09-168-595-148	Sequence 148, App
42	157.5	7.6	4	496	US-09-543-681A-6465	Sequence 6465, Ap
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44	156.5	7.5	3	1104	US-08-923-992A-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
US-08-973-462-8

; Sequence 8, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 0660-0125-0 PCT
; CURRENT APPLICATION NUMBER: US/08/973,462B
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: PCT/FR96/00894
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 8
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Polypeptide
US-08-973-462-8

  Query Match   9.6%; Score 198.5; DB 3; Length 1786;
  Best Local Similarity 22.2%; Pred. No. 3.6e-05;
  Matches 103; Conservative 105; Mismatches 172; Indels 85; Gaps 24;

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Qy   66 KDSL--YFFNIANSYLRFLFSD----------VRKLSGKYSKLLVPYLMEFSHKKEAEFEK 114
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Qy   115 ERFFNI----LEVEESYRNNLSDFNKRILKPAVEELKTLFENLKVERLKNGRVIKGYKFS 170
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